

Seq. No.	224031
Seq. ID	LIB3166-001-Q1-K1-H2
Method	BLASTX
NCBI GI	g3402704
BLAST score	344
E value	2.0e-32
Match length	119
% identity	66
NCBI Description	(AC004261) hypothetical protein [Arabidopsis thaliana]
Seq. No.	224032
Seq. ID	LIB3166-001-Q1-K1-H4
Method	BLASTX
NCBI GI	g421836
BLAST score	603
E value	8.0e-63
Match length	139
% identity	84
NCBI Description	G-box-binding factor GF14 - Arabidopsis thaliana >gi_553040 (M96855) GF14 [Arabidopsis thaliana]
Seq. No.	224033
Seq. ID	LIB3166-001-Q1-K1-H5
Method	BLASTX
NCBI GI	g2252631
BLAST score	158
E value	1.0e-10
Match length	63
% identity	49
NCBI Description	(U95973) hypothetical protein [Arabidopsis thaliana]
Seq. No.	224034
Seq. ID	LIB3166-001-Q1-K1-H6
Method	BLASTX
NCBI GI	g3319342
BLAST score	164
E value	2.0e-11
Match length	45
% identity	64
NCBI Description	(AF077407) similar to mitochondrial carrier proteins (Pfam: mit_carr.hmm, score: 79.74 and 42.50) [Arabidopsis thaliana]
Seq. No.	224035
Seq. ID	LIB3166-001-Q1-K1-H7
Method	BLASTX
NCBI GI	g1352076
BLAST score	162
E value	4.0e-11
Match length	134
% identity	33
NCBI Description	BETA-GALACTOSIDASE (LACTASE) >gi_144746 (M35107) beta-D-galactosidase (cbgA) [Clostridium acetobutylicum]
Seq. No.	224036
Seq. ID	LIB3166-001-Q1-K1-H8
Method	BLASTX


```
% identity      85
NCBI Description (AC004401) unknown protein [Arabidopsis thaliana]

Seq. No.       224042
Seq. ID        LIB3166-001-Q1-K3-B1
Method         BLASTX
NCBI GI        g3608485
BLAST score    597
E value        4.0e-62
Match length   117
% identity     95
NCBI Description (AF088915) proteasome beta subunit [Petunia x hybrida]
```

Seq. No.	224043
Seq. ID	LIB3166-001-Q1-K3-B11
Method	BLASTX
NCBI GI	g3859116
BLAST score	223
E value	6.0e-29
Match length	121
% identity	64
NCBI Description	(AF031609) unknown [Oryza sativa]

```
Seq. No.      224044
Seq. ID      LIB3166-001-Q1-K3-B2
Method       BLASTX
NCBI GI      g3790567
BLAST score   161
E value      5.0e-11
Match length  108
% identity    33
NCBI Description (AF078821) RING-H2 finger protein RHA1b [Arabidopsis thaliana]
```

```
Seq. No.          224045
Seq. ID           LIB3166-001-Q1-K3-B3
Method            BLASTX
NCBI GI           g1408471
BLAST score       455
E value           1.0e-45
Match length      102
% identity        79
NCBI Description   (U48938) actin depolymerizing factor 1 [Arabidopsis
                   thaliana] >gi_3851707 (AF102173) actin depolymerizing
                   factor 1 [Arabidopsis thaliana]
```

```
Seq. No.: 224046
Seq. ID: LIB3166-001-Q1-K3-B5
Method: BLASTX
NCBI GI: g1854386
BLAST score: 462
E value: 2.0e-46
Match length: 127
% identity: 69
NCBI Description: (AB001375) similar to soluble NSF attachment protein [Vitis vinifera]
```

```
Seq. No.      224047
Seq. ID      LIB3166-001-Q1-K3-B7
Method       BLASTX
NCBI GI      g886116
BLAST score   481
E value      1.0e-48
Match length  124
% identity    69
NCBI Description (U27609) TCH4 protein [Arabidopsis thaliana] >gi_2952473
              (AF051338) xyloglucan endotransglycosylase related protein
              [Arabidopsis thaliana]
```

Seq. No.	224048
Seq. ID	LIB3166-001-Q1-K3-B9
Method	BLASTX
NCBI GI	g2829918
BLAST score	511
E value	4.0e-52
Match length	121
% identity	80
NCBI Description	(AC002291) similar to "tub" protein gp_U82468_2072162 [Arabidopsis thaliana]

```
Seq. No.      224049
Seq. ID      LIB3166-001-Q1-K3-C1
Method       BLASTX
NCBI GI      g1545805
BLAST score   159
E value      5.0e-11
Match length  89
% identity   48
NCBI Description (D64052) cytochrome P450 like TBP [Nicotiana tabacum]
```

Seq. No.	224050
Seq. ID	LIB3166-001-Q1-K3-C11
Method	BLASTX
NCBI GI	g4262225
BLAST score	304
E value	6.0e-28
Match length	108
% identity	51
NCBI Description	(AC006200) putative phosphatidic acid phosphatase [Arabidopsis thaliana]

```
Seq. No.      224051
Seq. ID       LIB3166-001-Q1-K3-C2
Method        BLASTX
NCBI GI       g2459429
BLAST score    461
E value       3.0e-46
Match length   116
% identity     73
NCBI Description (AC002332) unknown protein [Arabidopsis thaliana]
```

```
Seq. No.      224052
Seq. ID      LIB3166-001-Q1-K3-C3
Method       BLASTX
```



```
Match length      115
% identity        49
NCBI Description  pectinesterase precursor - kidney bean
                  >gi_732913_emb_CAA59482_ (X85216) pectinesterase [Phaseolus
                  vulgaris]
```

```
Seq. No.          224115
Seq. ID           LIB3166-002-Q1-K1-F8
Method            BLASTX
NCBI GI           g2642448
BLAST score       384
E value           3.0e-37
Match length      118
% identity        29
NCBI Description   (AC002391) hypothetical protein [Arabidopsis thaliana]
                   >gi_3169187 (AC004401) hypothetical protein [Arabidopsis
                   thaliana]
```

[illegible][illegible][illegible][illegible]


```
BLAST score      366
E value          2.0e-41
Match length     132
% identity       61
NCBI Description (Z97338) similarity to hypothetical protein HYP1 -
Arabidopsis [Arabidopsis thaliana]
```

```
Seq. No.      224247
Seq. ID      LIB3166-006-P1-K1-B2
Method       BLASTX
NCBI GI      g125887
BLAST score   157
E value      1.0e-10
Match length  89
% identity    37
NCBI Description ANOTHER SPECIFIC LAT52 PROTEIN PRECURSOR
>gi_82092_pir_S04765 LAT52 protein precursor - tomato
>gi_295812_emb_CAA33854_ (X15855) LAT52 [Lycopersicon
esculentum]
```

```
Seq. No.          224248
Seq. ID           LIB3166-006-P1-K1-B4
Method            BLASTX
NCBI GI           g1332579
BLAST score       486
E value           2.0e-52
Match length      115
% identity        10
NCBI Description   (X98063) polyubiquitin [Pinus sylvestris]
```

Seq. No.	224249
Seq. ID	LIB3166-006-P1-K1-B5
Method	BLASTX
NCBI GI	g4218122
BLAST score	276
E value	1.0e-24
Match length	95
% identity	61
NCBI Description	(AL035353) putative protein [Arabidopsis thaliana]

```
Seq. No.      224250
Seq. ID       LIB3166-006-P1-K1-C1
Method        BLASTX
NCBI GI       g2213643
BLAST score   250
E value       1.0e-28
Match length  91
% identity    71
NCBI Description (U57338) glossy1 homolog [Oryza sativa]
```

Seq. No.	224251
Seq. ID	LIB3166-006-P1-K1-C11
Method	BLASTX
NCBI GI	g2065531
BLAST score	254
E value	5.0e-22
Match length	81

% identity 64
 NCBI Description (U78526) endo-1,4-beta-glucanase [*Lycopersicon esculentum*]

Seq. No. 224252
 Seq. ID LIB3166-006-P1-K1-C12
 Method BLASTX
 NCBI GI g1345787
 BLAST score 678
 E value 1.0e-71

Match length 134
 % identity 94
 NCBI Description CHALCONE SYNTHASE 2 (NARINGENIN-CHALCONE SYNTHASE 2)
 >gi_567937_dbj_BAA05641_ (D26594) chalcone synthase
 [*Camellia sinensis*]

Seq. No. 224253
 Seq. ID LIB3166-006-P1-K1-C4
 Method BLASTX
 NCBI GI g2244732
 BLAST score 446
 E value 2.0e-44

Match length 90
 % identity 94
 NCBI Description (D88413) endo-xyloglucan transferase [*Gossypium hirsutum*]

Seq. No. 224254
 Seq. ID LIB3166-006-P1-K1-C5
 Method BLASTX
 NCBI GI g2979551
 BLAST score 174
 E value 9.0e-13

Match length 57
 % identity 65
 NCBI Description (AC003680) putative receptor protein kinase [*Arabidopsis thaliana*]

Seq. No. 224255
 Seq. ID LIB3166-006-P1-K1-C7
 Method BLASTX
 NCBI GI g128190
 BLAST score 530
 E value 2.0e-54
 Match length 122
 % identity 80

NCBI Description NITRATE REDUCTASE 2 (NR2) >gi_66205_pir_RDNTNS nitrate
 reductase (NADH) (EC 1.6.6.1) nia-2 - common tobacco
 >gi_19891_emb_CAA32217_ (X14059) nitrate reductase
 [*Nicotiana tabacum*]

Seq. No. 224256
 Seq. ID LIB3166-006-P1-K1-D1
 Method BLASTX
 NCBI GI g4490341
 BLAST score 172
 E value 3.0e-12
 Match length 124
 % identity 39

Method	BLASTX
NCBI GI	g3046703
BLAST score	421
E value	4.0e-65
Match length	136
% identity	91
NCBI Description	(AL021749) protein kinase ADK1-like protein [Arabidopsis thaliana]

```
Seq. No.      224294
Seq. ID      LIB3166-007-P1-K1-B12
Method       BLASTX
NCBI GI      g3219353
BLAST score   453
E value      2.0e-47
Match length  135
% identity    73
NCBI Description (AF061514) manganese superoxide dismutase [Gossypium
                hirsutum]
```

```
Seq. No.      224295
Seq. ID.      LIB3166-007-P1-K1-B9
Method        BLASTX
NCBI GI       g4105696
BLAST score    275
E value       7.0e-25
Match length   57
% identity     93
NCBI Description (AF049870) beta tubulin 1 [Arabidopsis thaliana]
```

```
Seq. No.      224296
Seq. ID      LIB3166-007-P1-K1-C1
Method       BLASTX
NCBI GI      g4049399
BLAST score   158
E value      1.0e-10
Match length  101
% identity    37
NCBI Description (Y09581) FRO2 [Arabidopsis thaliana]
```

Seq. No.	224297
Seq. ID	LIB3166-007-P1-K1-C11
Method	BLASTX
NCBI GI	g3738291
BLAST score	241
E value	2.0e-20
Match length	95
% identity	46
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	224298
Seq. ID	LIB3166-007-P1-K1-C6
Method	BLASTX
NCBI GI	g2827634
BLAST score	163
E value	3.0e-11
Match length	91

NCBI GI g115833
 BLAST score 529
 E value 4.0e-54
 Match length 129
 % identity 78
 NCBI Description CHLOROPHYLL A-B BINDING PROTEIN CP24 10A PRECURSOR
 (CAB-10A) (LHCP) >gi_100195_pir_S11877 chlorophyll
 a/b-binding protein Cab10A - tomato >gi_170394 (M32605)
 a-binding protein [Lycopersicon esculentum]

Seq. No. 224376
 Seq. ID LIB3166-009-P1-K1-C1
 Method BLASTX
 NCBI GI g1702983
 BLAST score 325
 E value 3.0e-30
 Match length 110
 % identity 56
 NCBI Description AUXIN-REPRESSED 12.5 KD PROTEIN >gi_99855_pir_S11850
 hypothetical protein - garden strawberry
 >gi_22573_emb_CAA36676 (X52429) 12.5 kDa protein [Fragaria
 x ananassa] >gi_927034 (L44142) auxin-repressed protein
 [Fragaria ananassa]

Seq. No. 224377
 Seq. ID LIB3166-009-P1-K1-C11
 Method BLASTX
 NCBI GI g3395427
 BLAST score 169
 E value 6.0e-12
 Match length 103
 % identity 36
 NCBI Description (AC004683) unknown protein [Arabidopsis thaliana]

Seq. No. 224378
 Seq. ID LIB3166-009-P1-K1-C3
 Method BLASTX
 NCBI GI g1943751
 BLAST score 624
 E value 3.0e-65
 Match length 141
 % identity 89
 NCBI Description (U93845) Arabidopsis thaliana ER-type calcium pump
 protein, complete sequence >gi_2078292 (U96455) ER-type
 Ca2+-pumping ATPase; ECA1p [Arabidopsis thaliana]

Seq. No. 224379
 Seq. ID LIB3166-009-P1-K1-C6
 Method BLASTX
 NCBI GI g2245066
 BLAST score 402
 E value 3.0e-39
 Match length 134
 % identity 62
 NCBI Description (Z97342) Beta-Amylase [Arabidopsis thaliana]

Seq. No. 224380

000007-97043950

NCBI Description MADS BOX PROTEIN CMB1 >gi_695317 (L40404) MADS box protein
[Dianthus caryophyllus]

Seq. No. 224396
Seq. ID LIB3166-009-P1-K1-F9
Method BLASTX
NCBI GI g1345698
BLAST score 715
E value 6.0e-76
Match length 135
% identity 99

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE II PRECURSOR
(CAB-151) (LHCP) >gi_99601_pir_S20917 chlorophyll
a/b-binding protein - upland cotton
>gi_452314_emb_CAA38025_ (X54090) chlorophyll ab binding
protein [Gossypium hirsutum]

Seq. No. 224397
Seq. ID LIB3166-009-P1-K1-G10
Method BLASTX
NCBI GI g464707
BLAST score 535
E value 6.0e-55
Match length 114
% identity 90

NCBI Description 40S RIBOSOMAL PROTEIN S18 >gi_480908_pir_S37496 ribosomal
protein S18.A - Arabidopsis thaliana
>gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A
[Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701)
S18 ribosomal protein [Arabidopsis thaliana]
>gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein
[Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962)
S18 ribosomal protein [Arabidopsis thaliana]
>gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A
[Arabidopsis thaliana] >gi_3287678 (AC003979) Match to
ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A.
thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and
gb_R30430 come from this gene. [Arabidopsis thaliana]
>gi_4538910_emb_CAB39647.1 (AL049482) S18.A ribosomal
protein [Arabidopsis thaliana]

Seq. No. 224398
Seq. ID LIB3166-009-P1-K1-G11
Method BLASTX
NCBI GI g3176726
BLAST score 409
E value 4.0e-44
Match length 124
% identity 75

NCBI Description (AC002392) putative serine proteinase [Arabidopsis
thaliana]

Seq. No. 224399
Seq. ID LIB3166-009-P1-K1-G2
Method BLASTX
NCBI GI g2244749
BLAST score 616

NCBI Description (U81491) polyhomeotic 2 [Mus musculus]

Seq. No. 224503
 Seq. ID LIB3166-012-P1-K1-C7
 Method BLASTX
 NCBI GI g417192
 BLAST score 414
 E value 1.0e-40
 Match length 97
 % identity 78
 NCBI Description MONOCYTE CHEMOTACTIC PROTEIN 3 PRECURSOR (MCP-3) (MONOCYTE CHEMOATTRACTANT PROTEIN 3) (INTERCRINE/CHEMOKINE MARC) (FIC PROTEIN) >gi_57938_emb_CAA78169_(Z12297) intercrine [Mus musculus] >gi_547089_bbs_149941_(S71251) monocyte chemotactic protein-3, MCP-3, Marc/Fic protein [mice, macrophage cell line WEHI-3, Peptide, 97 aa] [Mus sp.]

Seq. No. 224504
 Seq. ID LIB3166-012-P1-K1-E11
 Method BLASTX
 NCBI GI g123651
 BLAST score 506
 E value 5.0e-62
 Match length 134
 % identity 96
 NCBI Description HEAT SHOCK COGNATE 71 KD PROTEIN >gi_111759_pir__S07197 heat shock cognate protein hsc73 - rat
 >gi_2119718_pir_JC4853 heat-shock protein 73 - mouse
 >gi_56379_emb_CAA68265_(Y00054) hsc73 [Rattus norvegicus]
 >gi_204667_(M11942) 70 kDa heat-shock-like protein [Rattus norvegicus] >gi_861213 (U27129) heat shock 73 protein [Mus musculus]

Seq. No. 224505
 Seq. ID LIB3166-012-P1-K1-E12
 Method BLASTX
 NCBI GI g3043917
 BLAST score 345
 E value 1.0e-32
 Match length 113
 % identity 63
 NCBI Description (AF029844) elongation factor 1-beta homolog [Mus musculus]

Seq. No. 224506
 Seq. ID LIB3166-012-P1-K1-E6
 Method BLASTX
 NCBI GI g114291
 BLAST score 272
 E value 1.0e-24
 Match length 53
 % identity 98
 NCBI Description ARGININOSUCCINATE SYNTHASE (CITRULLINE--ASPARTATE LIGASE) >gi_68637_pir_AJRTRS argininosuccinate synthase (EC 6.3.4.5) - rat >gi_55767_emb_CAA30999_(X12459) argininosuccinate synthetase (AA 1-412) [Rattus norvegicus] >gi_203016 (M36708) argininosuccinate synthetase [Rattus norvegicus]

```

Seq. No.      224507
Seq. ID       LIB3166-012-P1-K1-F10
Method        BLASTX
NCBI GI       g137475
BLAST score    729
E value        1.0e-77
Match length   139
% identity     99
NCBI Description VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT)
                (32 KD ACCESSORY PROTEIN) (P39) >gi_89602_pir_A32123
                H+-transporting ATPase (EC 3.6.1.35) polypeptide IV,
                vacuolar - bovine

```

Seq. No.	224508
Seq. ID	LIB3166-012-P1-K1-F11
Method	BLASTX
NCBI GI	g2833633
BLAST score	611
E value	1.0e-63
Match length	136
% identity	81
NCBI Description	(AC003108) Unknown gene product [Homo sapiens]

```
Seq. No.      224509
Seq. ID      LIB3166-012-P1-K1-F12
Method       BLASTX
NCBI GI      g543201
BLAST score   611
E value      1.0e-63
Match length  132
% identity    84
NCBI Description  collagen alpha 1(I) chain precursor - mouse (fragments)
```

```
Seq. No.      224510
Seq. ID      LIB3166-012-P1-K1-F3
Method       BLASTX
NCBI GI      g117505
BLAST score   193
E value      6.0e-15
Match length  71
% identity    56
NCBI Description  CALRETICULIN PRECURSOR (CRP55) (CALREGULIN) (HACBP) (ERP60)
                (CALBP) (CALCIUM-BINDING PROTEIN 3) (CABP3)
                >gi_627974_pir_JH0819 calreticulin precursor - rat
                >gi_55855_emb_CAA37446_ (X53363) precursor (AA -17 to 399)
                [Rattus norvegicus] >gi_488841_emb_CAA55890_ (X79327)
                calreticulin [Rattus norvegicus] >gi_1845572_dbj_BAA11345_
                (D78308) calreticulin [Rattus norvegicus]
```

Seq. No.	224511
Seq. ID	LIB3166-012-P1-K1-F4
Method	BLASTX
NCBI GI	g478811
BLAST score	232
E value	1.0e-19
Match length	74

[illegible]

(NID:g3123886) [Homo sapiens] >gi_3290172 (AF064824)
CARD-containing ICE associated kinase [Homo sapiens]
>gi_3342910 (AF078530) receptor interacting protein 2 [Homo
sapiens] >gi_4151948 (AF117829) serine/threonine kinase
RICK [Homo sapiens] >gi_4506537_ref_NP_003812.1_pRIP2_
UNKNOWN

Seq. No. 224516
Seq. ID LIB3166-012-P1-K1-H3
Method BLASTX
NCBI GI g809561
BLAST score 427
E value 3.0e-42
Match length 87
% identity 95
NCBI Description (X13055) gamma-actin [Mus musculus]

Seq. No. 224517
Seq. ID LIB3166-012-P1-K1-H6
Method BLASTX
NCBI GI g548747
BLAST score 312
E value 2.0e-32
Match length 71
% identity 92
NCBI Description 60S RIBOSOMAL PROTEIN L13A >gi_1363320_pir_A53204
ribosomal protein L13a - rat >gi_460776_emb_CAA48343_
(X68282) rat ribosomal protein L13a [Rattus norvegicus]

Seq. No. 224518
Seq. ID LIB3166-012-P1-K1-H7
Method BLASTX
NCBI GI g1213490
BLAST score 200
E value 3.0e-20
Match length 56
% identity 95
NCBI Description (U42719) C4 complement protein [Rattus norvegicus]

Seq. No. 224519
Seq. ID LIB3166-012-P1-K1-H8
Method BLASTX
NCBI GI g1173177
BLAST score 471
E value 1.0e-47
Match length 93
% identity 96
NCBI Description 40S RIBOSOMAL PROTEIN S10 >gi_1362933_pir_S55918 ribosomal
protein S10 - human >gi_550025 (U14972) ribosomal protein
S10 [Homo sapiens] >gi_1096944_prf_2113200G ribosomal
protein S10 [Homo sapiens]
>gi_4506679_ref_NP_001005.1_pRPS10_ ribosomal protein S10

Seq. No. 224520
Seq. ID LIB3166-013-P1-K1-A12
Method BLASTX
NCBI GI g2443757

NCBI Description (AC006340) unknown protein [Arabidopsis thaliana]

Seq. No.	224526
Seq. ID	LIB3166-013-P1-K1-B9
Method	BLASTX
NCBI GI	g2522534
BLAST score	185
E value	2.0e-14
Match length	86
% identity	48

NCBI Description (AF027302) TNF-alpha stimulated ABC protein [Homo sapiens]

Seq. No.	224527
Seq. ID	LIB3166-013-P1-K1-C1
Method	BLASTX
NCBI GI	g3269293
BLAST score	276
E value	1.0e-24
Match length	103
% identity	57

NCBI Description (AL030978) putative protein [Arabidopsis thaliana]

```
Seq. No.          224528
Seq. ID           LIB3166-013-P1-K1-C11
Method            BLASTX
NCBI GI           g2961378
BLAST score       574
E value           2.0e-59
Match length      143
% identity        39
```

NCBI Description (AL022141) putative protein [Arabidopsis thaliana]

Seq. No.	224529
Seq. ID	LIB3166-013-P1-K1-C5
Method	BLASTX
NCBI GI	g3021489
BLAST score	164
E value	2.0e-15
Match length	88
% identity	62

NCBI Description (AJ224934) histone H2B [*Lycopersicon esculentum*]

Seq. No.	224530
Seq. ID	LIB3166-013-P1-K1-C6
Method	BLASTX
NCBI GI	g3122388
BLAST score	610
E value	1.0e-63
Match length	131
% identity	31

NCBI Description WD-40 REPEAT PROTEIN MSI2 >gi_2394231 (AF016847) WD-40 repeat protein [Arabidopsis thaliana]

Seq. No.	224531
Seq. ID	LIB3166-013-P1-K1-C7
Method	BLASTX
NCBI GI	g4510345

E value 4.0e-30
 Match length 75
 % identity 87
 NCBI Description 60S RIBOSOMAL PROTEIN L9 >gi_971282_dbj_BAA07209_ (D38012)
 ribosomal protein L9 [Oryza sativa]

Seq. No. 224542
 Seq. ID LIB3166-013-P1-K1-F2
 Method BLASTX
 NCBI GI g4090533
 BLAST score 460
 E value 3.0e-46
 Match length 101
 % identity 82
 NCBI Description (U68215) ACC oxidase [Carica papaya]

Seq. No. 224543
 Seq. ID LIB3166-013-P1-K1-F6
 Method BLASTX
 NCBI GI g2146739
 BLAST score 262
 E value 8.0e-23
 Match length 118
 % identity 51
 NCBI Description hexokinase (EC 2.7.1.1) 1 - Arabidopsis thaliana >gi_881521
 (U28214) hexokinase 1 [Arabidopsis thaliana]

Seq. No. 224544
 Seq. ID LIB3166-013-P1-K1-F7
 Method BLASTX
 NCBI GI g400976
 BLAST score 426
 E value 1.0e-48
 Match length 108
 % identity 96
 NCBI Description RAS-RELATED PROTEIN RHA1 >gi_478671_pir_S23727 GTP-binding
 protein RHA1 - Arabidopsis thaliana >gi_16484_emb_CAA41863_
 (X59152) RHA1 [Arabidopsis thaliana]
 >gi_397594_emb_CAA80534_ (Z22958) GTP-binding protein
 [Arabidopsis thaliana]

Seq. No. 224545
 Seq. ID LIB3166-013-P1-K1-F9
 Method BLASTX
 NCBI GI g1888357
 BLAST score 499
 E value 1.0e-50
 Match length 123
 % identity 76
 NCBI Description (X98130) alpha-mannosidase [Arabidopsis thaliana]
 >gi_1890154_emb_CAA72432_ (Y11767) alpha-mannosidase
 precursor [Arabidopsis thaliana]

Seq. No. 224546
 Seq. ID LIB3166-013-P1-K1-G10
 Method BLASTX
 NCBI GI g2673910

NCBI GI	g3738325
BLAST score	403
E value	2.0e-39
Match length	110
% identity	71
NCBI Description	(AC005170) putative CaMB-channel protein [Arabidopsis thaliana]
Seq. No.	224590
Seq. ID	LIB3166-014-P1-K1-F1
Method	BLASTX
NCBI GI	g2924777
BLAST score	376
E value	3.0e-36
Match length	130
% identity	6
NCBI Description	(AC002334) putative receptor protein kinase [Arabidopsis thaliana]
Seq. No.	224591
Seq. ID	LIB3166-014-P1-K1-F10
Method	BLASTX
NCBI GI	g2662415
BLAST score	173
E value	2.0e-12
Match length	56
% identity	54
NCBI Description	(U97494) metallothionein-like protein [Prunus armeniaca]
Seq. No.	224592
Seq. ID	LIB3166-014-P1-K1-F2
Method	BLASTX
NCBI GI	g1351271
BLAST score	331
E value	6.0e-31
Match length	118
% identity	62
NCBI Description	TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM) >gi_1084309_pir__S52032 triose-phosphate isomerase (EC 5.3.1.1) precursor, chloroplast - spinach >gi_806312 (L36387) triosephosphate isomerase, chloroplast isozyme [Spinacia oleracea]
Seq. No.	224593
Seq. ID	LIB3166-014-P1-K1-F3
Method	BLASTX
NCBI GI	g1814424
BLAST score	582
E value	2.0e-60
Match length	134
% identity	79
NCBI Description	(U85254) homeodomain protein AHDP [Arabidopsis thaliana]
Seq. No.	224594
Seq. ID	LIB3166-014-P1-K1-F8
Method	BLASTX
NCBI GI	g115484

```

BLAST score      255
E value          3.0e-57
Match length     108
% identity       59
NCBI Description CALMODULIN 1 >gi_71684_pir_MCPZDC calmodulin - carrot
>gi_478632_pir_S22971 calmodulin - trumpet lily
>gi_541839_pir_S40301 calmodulin - Red bryony
>gi_2129970_pir_S70768 calmodulin CAM81 - garden petunia
>gi_18326_emb_CAA42423_ (X59751) calmodulin [Daucus carota]
>gi_19447_emb_CAA78301_ (Z12839) calmodulin [Lilium
longiflorum] >gi_169207 (M80836) calmodulin [Petunia
hybrida] >gi_308900 (L18912) calmodulin [Lilium
longiflorum] >gi_505154_emb_CAA43143_ (X60738) Calmodulin
[Malus domestica] >gi_535444 (U13882) calmodulin [Pisum
sativum] >gi_445602_prf__1909349A calmodulin [Daucus
carota]

```

```
Seq. No.          224595
Seq. ID           LIB3166-014-P1-K1-F9
Method            BLASTX
NCBI GI           g1709930
BLAST score       359
E value           2.0e-35
Match length      94
% identity        81
NCBI Description   PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE PRECURSOR (AIR
                  CARBOXYLASE) (AIRC) >gi_629656_pir_S43322
                  phosphoribosylaminoimidazole carboxylase (EC 4.1.1.21) -
                  moth bean >gi_349159 (L22584) 5-aminoimidazole
                  ribonucleotide carboxylase [Vigna aconitifolia]
```

Seq. No.	224596
Seq. ID	LIB3166-014-P1-K1-G1
Method	BLASTX
NCBI GI	g2809251
BLAST score	152
E value	2.0e-10
Match length	34
% identity	74
NCBI Description	(AC002560) F21B7.20 [Arabidopsis thaliana]

```
Seq. No.      224597
Seq. ID       LIB3166-014-P1-K1-G10
Method        BLASTX
NCBI GI       g2245087
BLAST score    218
E value        1.0e-17
Match length   86
% identity     44
NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]
```

```
Seq. No.      224598
Seq. ID      LIB3166-014-P1-K1-G5
Method       BLASTX
NCBI GI      g4127456
BLAST score   303
E value      1.0e-27
```


